



HHS Public Access

Author manuscript

J Neurochem. Author manuscript; available in PMC 2016 August 01.

Published in final edited form as:

J Neurochem. 2015 August ; 134(4): 629–641. doi:10.1111/jnc.13160.

STriatal-Enriched protein tyrosine Phosphatase (STEP) Regulates the PTP α /Fyn Signaling Pathway

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Abstract

The tyrosine kinase Fyn has two regulatory tyrosine residues that when phosphorylated either activate (Tyr⁴²⁰) or inhibit (Tyr⁵³¹) Fyn activity. Within the central nervous system, two protein tyrosine phosphatases (PTPs) target these regulatory tyrosines in Fyn. PTP α dephosphorylates Tyr⁵³¹ and activates Fyn, while STEP (STriatal-Enriched protein tyrosine Phosphatase) dephosphorylates Tyr⁴²⁰ and inactivates Fyn. Thus, PTP α and STEP have opposing functions in the regulation of Fyn; however, whether there is cross talk between these two PTPs remains unclear. Here, we used molecular techniques in primary neuronal cultures and *in vivo* to demonstrate that STEP negatively regulates PTP α by directly dephosphorylating PTP α at its regulatory Tyr⁷⁸⁹. Dephosphorylation of Tyr⁷⁸⁹ prevents the translocation of PTP α to synaptic membranes, blocking its ability to interact with and activate Fyn. Genetic or pharmacologic reduction of STEP₆₁ activity increased the phosphorylation of PTP α at Tyr⁷⁸⁹, as well as increased translocation of PTP α to synaptic membranes. Activation of PTP α and Fyn and trafficking of GluN2B to synaptic membranes are necessary for ethanol intake behaviors in rodents. We tested the functional significance of STEP₆₁ in this signaling pathway by ethanol administration to primary cultures as well as *in vivo*, and demonstrated that the inactivation of STEP₆₁ by ethanol leads to the activation of PTP α , its translocation to synaptic membranes, and the activation of Fyn. These findings indicate a novel mechanism by which STEP₆₁ regulates PTP α and suggest that STEP and PTP α coordinate the regulation of Fyn.

Keywords

STEP; PTP α ; dephosphorylation; ethanol administration; lipid rafts; dorsomedial striatum

Introduction

PTP α is a member of the receptor-type protein tyrosine phosphatases (PTPs) family and is characterized by a transmembrane domain and two intracellular catalytic domains (Sap *et al.* 1990; Wang and Pallen 1991; Paul and Lombroso 2003; Tonks 2006). It is expressed in many tissues, including the brain (Sap *et al.* 1990; Sahin *et al.* 1995). Several reports implicate PTP α in the regulation of integrin signaling, neurite outgrowth, oligodendrocyte

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The authors declare no conflicts of interest.

differentiation, and myelination through activation of its substrates Fyn and Src and modulation of signaling by NCAM (neural cell adhesion molecule) and CHL1 (close homolog of L1) (Bodrikov *et al.* 2005; Ye *et al.* 2008; Chen *et al.* 2006; Wang *et al.* 2009; Zeng *et al.* 2003).

PTP α activates Fyn by dephosphorylating its inhibitory Tyr residue (Y⁵³¹), allowing full activation of Fyn by auto-phosphorylation at a second regulatory Tyr (Y⁴²⁰) (Engen *et al.* 2008, Ingleby 2008). PTP α knockout (KO) mice have increased phosphorylation of Fyn at its inhibitory site (Y⁵³¹) and decreased Fyn activity (Ponniah *et al.* 1999; Su *et al.* 1999). PTP α KO mice show deficits in LTP as well as in learning and memory, consistent with a role of Fyn in regulating NMDA receptor trafficking to synaptic membranes (Skelton *et al.* 2003; Petrone *et al.* 2003).

Striatum-Enriched protein tyrosine Phosphatase (STEP) is widely expressed in multiple brain regions including the striatum, where two major isoforms, STEP₆₁ and STEP₄₆, are expressed (Lombroso *et al.* 1991; Boulanger *et al.* 1995). STEP₆₁ is enriched in membrane fractions while STEP₄₆ is enriched in cytosol fractions (Lombroso *et al.* 1993; Bult *et al.* 1996). STEP normally opposes the development of synaptic strengthening through dephosphorylation and inactivation of several kinases, including Fyn, as well as endocytosis of both NMDARs and AMPARs (Snyder *et al.* 2005; Zhang *et al.* 2008; Zhang *et al.* 2010; Zhang *et al.* 2011). Both high and low activities of STEP disrupt synaptic plasticity, and dysregulation of STEP activity is implicated in several neuropsychiatric and neurodegenerative disorders, including Alzheimer's disease (Zhang *et al.* 2010), schizophrenia (Carty *et al.* 2012), Parkinson's disease (Kurup *et al.* 2015), Huntington's disease (Saavedra *et al.* 2011; Gladding *et al.* 2012), post-traumatic stress disorder (Yang *et al.* 2012), and stress-induced anxiety disorders (Dabrowska *et al.* 2013).

Recent studies have indicated that PTP α is a critical determinant of ethanol consumption in rodent models (Gibb *et al.* 2011; Ben Hamida *et al.* 2013). PTP α , Fyn and STEP are all expressed in the striatum, and ethanol administration or binge drinking results in a PTP α -mediated activation of Fyn in the dorsomedial striatum (DMS) but not in the nearby dorsolateral striatum (DLS) or the nucleus accumbens (NAc). Moreover, viral-based knockdown of PTP α or Fyn in the DMS reduces ethanol intake in rats (Wang *et al.* 2007; Wang *et al.* 2010; Ben Hamida *et al.* 2013).

In contrast, recent findings have shown that STEP is phosphorylated and inactivated specifically in the DMS during ethanol administration, and that STEP KO mice or shRNA knockdown of STEP in the DMS increases ethanol consumption (Darcq *et al.* 2014; Legastelois *et al.* in press). STEP and PTP α act on one, and not the other, of the two regulatory tyrosines in Fyn (Bhandari *et al.* 1998; Nguyen *et al.* 2002). This led to our hypothesis that PTP α may be a novel substrate for STEP to coordinate the bidirectional regulation of Fyn by STEP and PTP α , which we test here using genetic, pharmacological, and molecular techniques. The results suggest that inactivation of STEP is required for activation of PTP α and Fyn both in rat primary corticostriatal cultures and *in vivo* after ethanol administration to mice.

Materials and reagents

All antibodies used in this study are listed in Table S1. Two dopamine D1 receptor agonists SKF-82958 and SKF-38393, the PKA inhibitor H-89, the PKA activator forskolin, and ethanol (190 proof) were purchased from Sigma-Aldrich (St. Louis, MO), while the selective phosphodiesterase 4 inhibitor rolipram was obtained from Tocris Biosciences (Ellisville, MO). Recombinant glutathione S-transferase (GST)-tagged PTP α protein was purchased from Sino Biological (Beijing, China), while active Fyn kinase was obtained from Millipore (Bedford, MA).

Animals

The wild type (WT) and STEP knockout (KO) male mice used in these experiments were 3–4 months of age, maintained on a C57BL/6 background, and generated at Yale University from heterozygous crosses as described previously (Venkitaramani *et al.* 2009). Experimental mice were group-housed with a maximum of 5 mice per cage in a climate-controlled facility with 12h light-dark cycle with access to food and water *ad libitum*. All experiments were carried out during the light phase of the cycle. All procedures were performed according to the National Institutes of Health Guide for the Care and Use of Laboratory Animals and were approved by the Institutional Animal Care and Use Committee at Yale University.

Tissue processing

Total homogenates and crude synaptic membrane fractions (P2) were obtained from WT and STEP KO mouse striatum following previous protocols (Xu *et al.* 2012). Briefly, tissues were homogenized in ice-cold TEVP buffer (in mM): 10 Tris, pH 7.4, 5 NaF, 1 Na₃VO₄, 1 EDTA, 1 EGTA and 320 sucrose with protease inhibitor cocktail (Roche, Indianapolis, IN). Aliquots of samples were saved as total homogenates. The remaining homogenates were centrifuged at 1000 g for 10 min and the supernatants were further spun at 12,000 g for 20 min to isolate crude synaptic membrane fractions (P2). The pellets were resuspended and briefly sonicated in RIPA buffer (Pierce Biotechnology, Rockford, IL) with protease and phosphatase inhibitors (Roche). Total protein concentrations were determined using a BCA protein assay kit (Pierce Biotechnology).

Immunoblotting

All procedures were previously described (Xu *et al.* 2012). Briefly, 30 μ g of samples were resolved on 8% SDS-PAGE and transferred to nitrocellulose membranes (Bio-Rad Laboratories, Richmond, CA). Blots were blocked, incubated with primary and secondary antibodies (Table S1) and developed using a Chemiluminescent Substrate kit (Pierce Biotechnology). Densitometry was performed and analyzed using Genetools program (Syngene, Cambridge, UK). All phospho-protein levels were normalized to total protein levels and then to the loading control β -actin.

GST fusion proteins and pull-down assays

PCR-amplified open reading frames of WT STEP₆₁, the substrate trapping STEP₆₁ C472S, or the substrate trapping STEP₄₆ C300S were inserted into pGEX4T1 vectors (GE

Lifesciences, Piscataway, NJ). The substrate-trapping STEP protein has a point mutation at its critical cysteine within the phosphatase domain, rendering STEP inactive. This variant of STEP still binds to its substrates, but does not release them, as dephosphorylation is required for release; these constructs have been used to identify STEP substrates in the past (Nguyen *et al.* 2002; Paul *et al.* 2003; Xu *et al.* 2012). Glutathione S-transferase (GST) fusion proteins were expressed in *E. coli* BL21 (DE3) and purified on glutathione sepharose (GE Lifesciences) as described (Xu *et al.* 2012). For pull-down assays, GST fusion proteins were conjugated to glutathione sepharose beads and incubated with mouse striatal lysates overnight at 4 °C. STEP interacting proteins were probed with specific antibodies.

Immunoprecipitation

WT and STEP KO mouse striatum or rat primary corticostriatal neurons were lysed in immunoprecipitation (IP) buffer (in mM): 10 Tris-HCl pH 7.4, 150 NaCl, 1% Triton X-100, 1 EDTA and 1 EGTA with protease and phosphatase inhibitor cocktail (Roche). Lysates were incubated with anti-STEP or anti-PTP α antibodies overnight at 4 °C. On the second day, Protein A/G plus agarose beads (Santa Cruz Biotechnology, Santa Cruz, CA) were added for 4 h. Beads were washed 3 times and resuspended in 2 \times Laemmli buffer (Bio-Rad Laboratories) and subjected to SDS-PAGE and western blotting.

Dephosphorylation of PTP α by STEP *in vitro*

Recombinant GST-PTP α was phosphorylated at pY⁷⁸⁹ by Fyn kinase *in vitro* in kinase assay buffer (in mM): 50 Tris-HCl, pH 7.5, 0.1 EGTA, 10 MgCl₂, 500 μ M ATP for 30 min at 30 °C. Total reaction volume of kinase assay was 30 μ l. Adding EDTA/EGTA mix to a final concentration of 5 mM stopped the phosphorylation reaction. GST-pY⁷⁸⁹ PTP α was then incubated with active WT GST-STEP₆₁ or inactive GST-STEP₆₁ C472S (0–200 nM) in phosphatase assay buffer (in mM): 25 HEPES pH 7.3, 5 EDTA, 10 DTT for 30 min at 30 °C. The amount of pY⁷⁸⁹ PTP α remaining was visualized using the phospho-specific antibody to this site.

Primary neuronal cultures and treatments

Primary corticostriatal cultures were derived from rat Sprague-Dawley E18 embryos (Jackson Laboratory, Bar Harbor, Maine) or from mouse STEP KO E18 embryos as described (Xu *et al.* 2012). Both male and female embryos were used in this study. Cultures were treated with SFK-82958 (10 μ M, 30 min), SFK-38393 (10 μ M, 30 min), forskolin (100 μ M, 10 min) or rolipram (1 μ M, 30 min). In some cases, cultures were pre-treated with the PKA inhibitor H-89 (10 μ M, 30 min) followed by SKF-82958 or SKF-38393 stimulations. After treatments, neurons were lysed in RIPA buffer (Pierce Biotechnology) with protease and phosphatase inhibitors (Roche). Lysates were spun at 1000 g for 10 min and supernatants were saved for further analyses.

Viral infection

A recombinant adeno-associated virus of mixed serotype 1/2 (AAV1/2) was custom made (GeneDetect LTD, Auckland, New Zealand). Viruses contained either HA-tagged STEP₆₁ or a HA-tagged empty vector, both with a hybrid chicken β -actin/CMV enhancer (CAG)

promoter, rAAV2 inverted terminal repeat, a cis-acting woodchuck post-transcriptional regulatory element, and a bovine growth hormone polyadenylation signal sequence. The titers of the viral preparations were $>1 \times 10^{12}$ genomic particles/ml. At DIV (days in vitro) 5, STEP KO mouse cultures were infected with AAV1/2-STEP₆₁ or AAV1/2-control vector for 10 days.

Lentivirus-based STEP shRNA (LV-STEP; a gift from Thomas Lanz, Pfizer Research & Development, Cambridge, MA) was made as described (Reinhart *et al.* 2014). The target sequence for STEP shRNA was: 5'-GCATGACTCTTTGGCAACATG-3' using a loop sequence of 5'-TTCAAGAGA-3'. Control shRNA (5'-AATTCAGCGGGAGCCACCTGA-3') was designed to target firefly luciferase, which is not homologous to any endogenous rat transcripts and therefore should work as a scrambled sequence. Validation of STEP shRNA and control shRNA was described (Reinhart *et al.* 2014; Lanz *et al.* 2013). Rat corticostriatal cultures were infected with LV-STEP or a luciferase control at DIV 7 for 7 days.

Ethanol administration

Male C57BL/6 mice (2–3 months, Jackson Laboratory) were injected intraperitoneally with saline or 20% ethanol (190 proof diluted in saline, 2 g/kg) and sacrificed 15 min post injection. For repeated treatment, mice were administered with saline or 20% ethanol (2 g/kg, i.p.) once daily for 7 days and sacrificed 16 h after the last injection. In some experiments, STEP KO mice (C57BL/6 background) were administered with saline or 20% ethanol (190 proof diluted in saline, 2 g/kg, i.p.) for 15 min. The DMS, DLS and NAc were microdissected and kept at -80 °C until use.

Lipid rafts isolation

A detergent-free protocol was used to isolate lipid rafts from mouse brain as described (Persaud-Sawin *et al.* 2009). Briefly, WT or STEP KO mouse DMS were collected after ethanol administration. Tissues were homogenized in lysis buffer, as described above. Homogenates were centrifuged at 1000 g for 10 min and supernatants were saved. The pellets were resuspended in lysis buffer and passed through a 23-gauge needle, followed by 1000 g spin for 10 min. The second supernatant was pooled with the first one and 250 μ l of pooled supernatant was mixed gently with equal amount of 80% sucrose in lysis buffer. Five hundred μ l of 30% sucrose was layered on top, followed by a third layer of 5% sucrose. Gradients were centrifuged at 200,000 g in a Beckman Coulter TLA120.1 rotor for 18 h at 4 °C. Twelve sequential fractions (120 μ l) were collected and assayed using immunoblotting.

Statistical analysis

All experiments were repeated at least three times. Data were expressed as means \pm SEM. Statistical significance was determined by Student's *t*-test or one-way ANOVA with *post hoc* Tukey's test. For co-immunoprecipitation and rafts isolation experiments in WT and STEP KO mice, a two-way ANOVA with genotype and treatment as main factors followed by *post hoc* Tukey's test was used to determine statistical significance, with *p* values < 0.05 considered significant.

Results

Increased phosphorylation of PTP α at Tyr⁷⁸⁹ in STEP KO mouse brains

Previous studies have established that loss of STEP leads to elevated basal tyrosine phosphorylation of all STEP substrates identified to date (Venkitaramani *et al.* 2009; Nguyen *et al.* 2002; Xu *et al.* 2012). We reasoned that if PTP α is a novel substrate for STEP, there would be an increase in the tyrosine phosphorylation of PTP α at Y⁷⁸⁹ in STEP KO mouse brains. There was a significant increase in the phosphorylation of this site (1.47 ± 0.12 of WT, $p < 0.05$), with no change in total PTP α level ($p > 0.05$, Fig. 1a). We then examined the phosphorylation of the two regulatory tyrosine sites in Fyn. STEP KO brains showed elevated tyrosine phosphorylation of Fyn at pY⁴²⁰ (1.55 ± 0.13 of WT, $p < 0.01$), consistent with previous findings that this site is directly regulated by STEP (Nguyen *et al.* 2002). In contrast, there was a significant decrease in Fyn phosphorylation at the PTP α site (pY⁵³¹: 0.60 ± 0.10 of WT, $p < 0.05$), consistent with an increase in PTP α activity (Ponniah *et al.* 1999; Su *et al.* 1999).

These results indicate that PTP α Y⁷⁸⁹ phosphorylation is increased in STEP KO samples. We next determined whether re-expressing STEP₆₁ into STEP KO cultures was sufficient to reverse the increase in PTP α phosphorylation. Pilot studies using adeno-associated virus1/2 (AAV1/2)-STEP₆₁ confirmed a robust STEP₆₁ expression when corticostriatal cultures were infected with AAV1/2-STEP₆₁ but not with vector alone (Fig. S1). The doublet present is due to differential phosphorylation of STEP₆₁ (Paul *et al.* 2000). Restoration of STEP₆₁ into STEP KO cultures led to significant decreases in the Tyr phosphorylation of PTP α and a concomitant increase in the phosphorylation of the PTP α site on Fyn (PTP α pY⁷⁸⁹: 0.71 ± 0.08 of control; Fyn pY⁵³¹: 1.33 ± 0.10 of control, p values < 0.05 , Fig. 1b). In addition, re-expression of STEP₆₁ into these cultures resulted in a decrease in the Tyr phosphorylation of Fyn at the STEP₆₁ site (Fyn pY⁴²⁰: 0.72 ± 0.06 of control, $p < 0.05$).

Phospho-Fyn antibodies also recognize other Src family kinases, including Src at equivalent phosphorylation sites. To determine whether the changes in Fyn phosphorylation were specific to Fyn, we immunoprecipitated Fyn and Src from STEP KO lysates with specific antibodies, followed by probing with phospho-antibodies. We found alterations in Fyn phosphorylation but not Src (Fig. S2). These results are in agreement with previous findings showing Src is not a direct target of STEP (Nguyen *et al.* 2002).

PTP α translocation to synaptic membrane fractions is required for full activation of Fyn (Gibb *et al.* 2011). Thus we next investigated the phosphorylation levels of PTP α and Fyn in synaptic fractions of striatum from WT and STEP KO mice. There was a significantly higher basal level of phospho-PTP α in the striatum of STEP KO mice (1.42 ± 0.15 of WT, $p < 0.05$), as well as an increase in total PTP α (Fig. 1c). The higher levels of pPTP α in synaptic membranes correlated with a decrease in the Tyr phosphorylation of the PTP α site in Fyn, while the Tyr phosphorylation of the STEP site was increased (PTP α site on Fyn (Y⁵³¹): 0.75 ± 0.03 of WT; STEP site on Fyn (Y⁴²⁰): 1.44 ± 0.15 of WT, p values < 0.05), with no changes in total Fyn levels in P2 fractions. In addition, there were no changes in the Tyr phosphorylation of PTP α and Fyn in homogenates or P2 fractions from cerebellum (Fig. S3), a brain region in which STEP is not expressed.

STEP₆₁ binds to and dephosphorylates PTP α at Tyr⁷⁸⁹

We next examined whether there is physical association between STEP₆₁ and PTP α . We took advantage of a substrate-trapping form of STEP₆₁ that contains a mutation of the catalytic site cysteine to a serine residue that inactivates STEP₆₁. This mutated isoform of STEP binds to its substrates but does not release them, as release requires dephosphorylation of substrates (Xu *et al.* 2012; Nguyen *et al.* 2002). The N-terminal unique sequence of STEP₆₁ contributes to the binding of some substrates (Fyn and Pyk2) (Nguyen *et al.* 2002; Xu *et al.* 2012), while STEP₄₆ preferentially binds to ERK2 and p38. Here we detected binding of endogenous PTP α to recombinant STEP₆₁ C/S but not to STEP₄₆ C/S. Positive controls included Fyn and ERK2 (Fig. 2a). We confirmed that there was no binding of either STEP isoform to Src (Nguyen *et al.* 2002). These results indicate that STEP₆₁, and not STEP₄₆, interacts with PTP α *in vitro*.

To investigate possible associations *in vivo*, we performed reciprocal immunoprecipitation (IP) of STEP or PTP α from WT and STEP KO mouse striatal lysates. STEP IP co-precipitated PTP α and Fyn from WT lysates but not from STEP KO lysates (Fig. 2b, replicates shown in Fig. S4), while IgG alone and an antibody to Src were used as negative controls. A two-way ANOVA revealed that there was a main effect of treatment (IgG vs anti-STEP: $F(1,8) = 44.22, p < 0.001$) and genotype (WT vs KO: $F(1,8) = 40.46, p < 0.001$) with an interaction between these factors ($F(1,8) = 38.77, p < 0.001$, Fig. S4a). Association was confirmed with the reciprocal IP; STEP₆₁ co-precipitated with PTP α from WT lysates but not from STEP KO lysates (treatment: $F(1,8) = 12.00, p < 0.01$; genotype: $F(1,8) = 14.19, p < 0.01$) and interaction: ($F(1,8) = 13.68, p < 0.01$, Fig. S4b). The absence of STEP did not affect the known interaction between PTP α and Fyn (Bhandari *et al.* 1998) (Fig. 2c, Fig. S4b). Reciprocal IP was also performed with rat primary corticostriatal cultures to confirm the interaction between STEP₆₁ and PTP α (Fig. S5).

We next examined whether STEP₆₁ could dephosphorylate PTP α . We phosphorylated recombinant PTP α using Fyn and confirmed the phosphorylation using a phospho-specific antibody to Y⁷⁸⁹ (Fig. 2d). We also assayed PTP α phosphatase activity using para-nitrophenyl phosphate (pNPP) and determined that phosphorylation of PTP α by Fyn did not alter PTP α activity (data not shown). We then incubated phosphorylated PTP α with active WT GST-STEP₆₁ or inactive GST-STEP₆₁ C/S proteins and saw a dose-dependent dephosphorylation of PTP α by active but not inactive STEP₆₁ (Fig. 2e). Together, these results indicate that PTP α is a direct substrate of STEP₆₁.

Regulation of PTP α by STEP in primary cell cultures

If PTP α is a substrate for STEP, we reasoned that the tyrosine phosphorylation level of PTP α would change as we modulated STEP₆₁ activity. It is known that D1 dopamine receptor (D1R) stimulation results in a PKA-mediated phosphorylation of STEP at serine²²¹ (Ser²²¹) within the substrate-binding domain (kinase interacting motif, KIM) (Paul *et al.* 2000). Phosphorylation at this regulatory serine prevents STEP from interacting with its substrates. We treated corticostriatal cultures with two D1R agonists, SKF-82958 and SKF-38393, and showed the expected increase in STEP₆₁ phosphorylation (SKF-82958: 1.46 ± 0.14 of control; SKF-38393: 1.43 ± 0.15 of control, p values < 0.05) (Fig. 3a). We

also found an increase in pY⁷⁸⁹ PTP α levels when STEP₆₁ was phosphorylated at Ser²²¹ (inactive STEP₆₁) (SKF-82958: 1.53 ± 0.19 of control; SKF-38393: 1.43 ± 0.11 of control, p values < 0.05). Phosphorylation levels of the STEP site in Fyn (Y⁴²⁰) was also increased (SKF-82958: 1.55 ± 0.17 of control; SKF-38393: 1.50 ± 0.06 of control, p values < 0.05). Moreover, there was a decrease in the phosphorylation of the PTP α site on Fyn (pY⁵³¹) (SKF-82958: 0.72 ± 0.07 of control; SKF-38393: 0.64 ± 0.11 of control, p values < 0.05), presumably due to enhanced dephosphorylation by PTP α . Total protein levels did not alter during drug treatments. As expected, the PKA inhibitor H-89 blocked these effects (Fig. 3a).

To further confirm these results, we activated PKA using forskolin and rolipram in corticostriatal cultures. Both forskolin and rolipram induced robust increases in phosphorylation of STEP₆₁ at Ser²²¹ (Fsk: 2.13 ± 0.18 of control, $p < 0.01$; Rol: 1.45 ± 0.08 of control, $p < 0.05$) and subsequent increases in the Tyr phosphorylation of PTP α (Fsk: 1.46 ± 0.18 of control; Rol: 1.50 ± 0.18 of control, p values < 0.05) and Fyn at the STEP site (Y⁴²⁰) (Fsk: 1.76 ± 0.24 of control; Rol: 1.71 ± 0.21 of control, p values < 0.05) (Fig. 3b). In addition, forskolin and rolipram treatments led to a significant decrease in the phosphorylation of the PTP α site on Fyn (Y⁵³¹), consistent with increased activation of PTP α (Fsk: 0.62 ± 0.09 of control; Rol: 0.59 ± 0.12 of control, p values < 0.05).

Next we used gene-specific knockdown to confirm the regulation of PTP α by STEP₆₁. Lentiviral-STEP shRNA was added to cultures (DIV 5 days) for 7 days as described (Reinhart *et al.* 2014) and resulted in a significant decrease in STEP₆₁ expression compared to control (0.24 ± 0.03 of control, $p < 0.01$, Fig. 4). We observed an increase in PTP α phosphorylation and a decrease in the Tyr phosphorylation of the PTP α site on Fyn (PTP α (pY⁷⁸⁹): 1.37 ± 0.08 of control; Fyn (pY⁵³¹): 0.77 ± 0.08 of control, p values < 0.05). Moreover, the knockdown of STEP₆₁ expression correlated with an increase in the Tyr phosphorylation of the STEP₆₁ site on Fyn (pY⁴²⁰) (1.36 ± 0.09 of control, $p < 0.05$). Taken together, these knockdown experiments confirmed the earlier results of acute pharmacological inactivation of STEP.

Ethanol administration leads to phosphorylation and inactivation of STEP₆₁, and subsequent translocation of PTP α to lipid rafts fraction

We next examined the functional significance of the regulation of PTP α by STEP₆₁. PTP α and Fyn both play a critical role in modulating ethanol (EtOH) intake. EtOH administration in rodents leads to activation of Fyn and an increase in the localization of PTP α within synaptic membranes specifically in the dorsomedial striatum (DMS) (Gibb *et al.* 2011; Ben Hamida *et al.* 2013). EtOH treatment also results in the phosphorylation and inactivation of STEP₆₁, as well as activation of Fyn and the phosphorylation of the Fyn target GluN2B, again specifically in the DMS, but not in the adjacent dorsolateral striatum (DLS) or nucleus accumbens (NAc) (Darq *et al.* 2014). Given these findings, we asked if STEP₆₁ modulated PTP α phosphorylation and translocation during ethanol administration.

We employed two paradigms for these experiments: acute ethanol injection and repeated ethanol injections in mice followed by a withdrawn period (Gibb *et al.* 2011; Ben Hamida *et al.* 2013). C57BL/6 mice were acutely injected with ethanol (2 g/kg, i.p.) and sacrificed 15 min later. Synaptic membrane fractions from DMS, DLS or NAc were processed for levels

of STEP₆₁ and its substrates. Consistent with previous findings (Gibb *et al.* 2011), we observed an increased localization of PTP α in the synaptic membrane fractions in DMS (1.40 ± 0.18 of saline, $p < 0.05$) but not in DLS or NAc (Fig. 5a). We also confirmed an increase in STEP₆₁ phosphorylation following ethanol injection in DMS (1.58 ± 0.27 of saline, $p < 0.05$) (Darcq *et al.* 2014). Both total and phospho-PTP α at Y⁷⁸⁹ increased in synaptic membrane fractions (Fig. 5a), supporting the observation that phosphorylation at this site is required for PTP α trafficking to membrane fractions (Maksumova *et al.* 2005; Gibb *et al.* 2011). Consistent with the enhanced trafficking of PTP α to synaptic fractions, we found a decrease in the phosphorylation of the PTP α site in Fyn (Y⁵³¹: 0.66 ± 0.10 of saline, $p < 0.05$), and an increase in the phosphorylation of the STEP₆₁ site in Fyn (Y⁴²⁰: 1.46 ± 0.18 of saline, $p < 0.05$), possibly due to inactivation of STEP₆₁. We observed none of these changes in the DLS or NAc (Fig. 5b and c). These results suggest a model of synergistic regulation of Fyn by STEP and PTP α in DMS upon acute EtOH administration.

Previous studies showed that repeated ethanol exposure increased the phosphorylation of Fyn at Y⁴²⁰, but decreased the phosphorylation of Fyn at Y⁵³¹ (Wang *et al.* 2010). We followed a similar protocol with repeated ethanol injection (2 g/kg, i.p. daily for 7 days followed by 16 h withdrawn) and examined the effects of ethanol treatment on STEP₆₁, PTP α and Fyn in the DMS, DLS and NAc (Fig. S6). We confirmed the changes in phosphorylation of Fyn, finding increased pY⁴²⁰ Fyn and decreased pY⁵³¹ Fyn only in the DMS (pY⁴²⁰: 1.46 ± 0.15 of saline; pY⁵³¹: 0.66 ± 0.08 of saline, p values < 0.05). Moreover, we found increased phosphorylation (inactivation) of STEP₆₁ and a concomitant increased phosphorylation of PTP α at Y⁷⁸⁹ and translocation of PTP α to synaptic fractions in DMS (pSTEP: 1.57 ± 0.21 of saline; PTP α : 1.39 ± 0.17 of saline; pY⁷⁸⁹ PTP α : 1.47 ± 0.19 of saline, p values < 0.05). These results suggest that inactivation of STEP₆₁ may be a required for PTP α phosphorylation and translocation to synaptic membrane compartments, resulting in maximal activation of Fyn.

To follow translocation of PTP α into lipid rafts fraction upon EtOH administration, we used a detergent-free protocol (Persaud-Sawin *et al.* 2009). We first validated our preparation by two criteria commonly used in the field: (1) presence or absence of marker proteins and (2) high cholesterol and low protein content of the rafts fraction (Persaud-Sawin *et al.* 2009). Flotillin-1, a marker present in lipid rafts, was enriched and correlated with high cholesterol and low protein content in fractions 3 and 4 (Fig. S7). In contrast, the transferrin receptor (TfR), which is excluded from lipid rafts, was recovered mainly in fractions 10–12, and correlated with high protein and low cholesterol content (Fig. S7). Consistent with previous findings (Gibb *et al.* 2011), we confirmed the expression of Fyn in both lipid rafts and non-rafts fractions (Fig. 6a). In addition, we found that PTP α and STEP₆₁ were primarily in non-rafts fractions at baseline in mouse DMS. We acutely administrated mice with EtOH (2 g/kg, i.p.) or vehicle for 15 min. EtOH administration led to PTP α re-distribution into rafts fractions, without altering the localization of STEP₆₁ or Fyn (Fig. 6a).

If EtOH-induced phosphorylation and inactivation of STEP₆₁ promoted PTP α translocation to the rafts fractions in WT mice, we reasoned that PTP α might be constitutively localized in the rafts fractions derived from STEP KO mice. We found that PTP α was present in both rafts and non-rafts fractions under baseline conditions (Fig. 6b). A two-way ANOVA

analysis of PTP α expression in the rafts showed a main effect of treatment (Sal vs EtOH: $F(1,16) = 17.46, p < 0.001$) and genotype (WT vs KO: $F(1,16) = 12.48, p < 0.01$) with an interaction between these factors ($F(1,16) = 17.46, p < 0.001$, Fig. 6c). However, no changes were observed in PTP α levels in the non-rafts fractions (treatment: $F(1,16) = 0.76, p = 0.39$; genotype: $F(1,16) = 0.74, p = 0.40$; interaction: $F(1,16) = 0.06, p = 0.80$, Fig. 6c). Together, these results suggest STEP₆₁ is involved in PTP α translocation to lipid rafts upon EtOH administration.

Discussion

Here we establish that PTP α is a novel substrate for STEP₆₁ and that STEP₆₁ binds to and dephosphorylates PTP α at Y⁷⁸⁹. We used STEP KO mice, knockdown of STEP₆₁, and pharmacological interventions to lower STEP activity, and find increased phosphorylation of PTP α at Y⁷⁸⁹ on PTP α , while overexpression of STEP₆₁ results in a decreased phosphorylation of PTP α . The data indicate that inactivation of STEP₆₁ contributes to the increased tyrosine phosphorylation of PTP α and subsequent translocation into lipid raft fractions, leading to the activation of Fyn. We also demonstrated the functional significance of this pathway by showing that it is activated specifically in the DMS during ethanol administration.

PTP α is a receptor-type protein tyrosine phosphatase that is widely expressed in many tissues. Within the CNS, PTP α is implicated in the development of synaptic plasticity and long-term potentiation (LTP) through its ability to activate Fyn and potentiate NMDA receptor signaling. In support of this, PTP α KO mice have decreased Fyn activity and deficits in memory consolidation and LTP (Skelton *et al.* 2003; Petrone *et al.* 2003). PTP α is regulated by several mechanisms, including oxidation-induced dimerization and inactivation (Jiang *et al.* 1999; Yang *et al.* 2007), phosphorylation (den Hertog *et al.* 1994; Zheng *et al.* 2000; Zheng *et al.* 2002), and translocation between cytoplasm and lipid rafts (Maksumova *et al.* 2005; Gibb *et al.* 2011). We find an elevation of PTP α pY⁷⁸⁹ in dorsal striatum but not in cerebellum of STEP KO mice, consistent with the absence of STEP protein in the cerebellum. It would be interesting to determine whether PTP-SL (Pulido *et al.* 1998), a closely related PTP to STEP that is present in cerebellum, similarly regulates PTP α in that brain region.

Early reports suggested that pY⁷⁸⁹ provides a binding site for the SH2 domain of Src/Fyn, thus facilitating the activation of Src/Fyn by removing its intramolecular inhibition (Zheng *et al.* 2000; Bhandari *et al.* 1998); however, there are conflicting results, as site-directed mutation did not affect downstream Src signaling, nor was the Y⁷⁸⁹ site involved in mediating the interaction of PTP α with Src/Fyn (Chen *et al.* 2006; Lammers *et al.* 2000; Vacaru and den Hertog 2010). Other studies suggest that the phosphorylation at Tyr⁷⁸⁹ is needed for Grb2 binding and subsequent activation of MAPK/ERK signaling (den Hertog *et al.* 1994; den Hertog and Hunter 1996; Su *et al.* 1996). The direct modulation of intrinsic phosphatase activity by phosphorylation at Y⁷⁸⁹ is also under debate. Some report that dephosphorylation of this site affects PTP α activity (Maksumova *et al.* 2007), while others suggest that it does not (den Hertog *et al.* 1994; Su *et al.* 1996; Zheng *et al.* 2000). Our *in vitro* assay indicate that phosphorylation of PTP α at Y⁷⁸⁹ does not alter its phosphatase activity using pNPP as substrate.

The possible regulation of PTP α translocation by pY⁷⁸⁹ is relevant to this study. Previous findings suggested that upon integrin activation, PTP α translocates to focal adhesions in an Y⁷⁸⁹ dependent-manner (Lammers *et al.* 2000; Sun *et al.* 2012), and translocation is critical for full activation of Fyn (Maksumova *et al.* 2005; Vacaresse *et al.* 2008). Ethanol administration was shown to induce translocation of PTP α to synaptic membrane fractions (Gibb *et al.* 2011). Consistent with these reports, we find elevated PTP α levels in synaptic membranes of STEP KO striatum, with a proportional increase in pY⁷⁸⁹. Acute or repeated ethanol administration also increased the phosphorylation and inactivation of STEP₆₁, increased the phosphorylation of the STEP target PTP α , and increased trafficking of PTP α to synaptic membranes. Moreover, using a lipid rafts extraction protocol, we show that acute EtOH resulted in the re-distribution of PTP α to rafts fractions, where Fyn is enriched, in WT mice. In support of our hypothesis, we find increased localization of PTP α in rafts fractions under baseline conditions in STEP KO mice and EtOH administration did not induce a further translocation of PTP α in STEP KO mice.

These data suggest that decreased STEP₆₁ activity leads to increased phosphorylation of PTP α at Y⁷⁸⁹ and subsequent translocation of PTP α to lipid rafts, facilitating its interaction with Fyn and NMDA receptors, both critical players in regulating EtOH-related behaviors (Wang *et al.* 2007; Ben Hamida *et al.* 2013). Interestingly, a recent report shows that STEP KO mice have more EtOH consumption (Legastelois *et al.* in press), possibly due to enhanced PTP α , Fyn and NMDAR signaling in rafts fractions in STEP KO mice. The molecular mechanisms that underlie PTP α translocation are not well understood. Several SH2-domain containing adaptor proteins are present at focal adhesions (Boivin *et al.* 2013; Shen and Guan 2004) or associated with raft targeting proteins (Liu *et al.* 2002; Kimura *et al.* 2001; Limpert *et al.* 2007), thus it is possible that phosphorylated PTP α is recruited by these adaptor proteins to neuronal lipid rafts via pY⁷⁸⁹-SH2 domain interaction during ethanol administration.

One unanswered question is what determines the brain region specificity of ethanol-induced phosphorylation and inactivation of STEP₆₁ in the DMS, but not in DLS or NAc. STEP₆₁ is phosphorylated by PKA at a regulatory serine residue within its KIM domain upon dopamine D1 receptor (D1R) activation (Paul *et al.* 2000), while PP2B/PP1 dephosphorylates and activates STEP₆₁ (Snyder *et al.* 2005; Valjent *et al.* 2005). Activation of D1R and PKA by ethanol is well documented; however, activation of PKA by ethanol is not restricted to the DMS (Di Chiara and Imperato 1988; Asyyed *et al.* 2006; Ron and Messing 2013). Studies are needed to clarify the mechanism for the differential regulation of STEP in distinct brain regions, such as DMS, after EtOH administration. Although recent studies have suggested that subregions of the striatum are involved in the regulation of distinct aspects of alcohol abuse (Chen *et al.* 2011), the mechanisms by which this occurs remain unclear. The differential regulation of STEP within specific brain regions has been previously reported. For example, STEP levels are elevated in striatum in human sporadic Parkinson's disease and in MPTP-treated mouse models, but not in cortex (Kurup *et al.* 2015), while STEP levels are elevated in cortex of patients with Alzheimer's disease and schizophrenia (Zhang *et al.* 2010; Carty *et al.* 2012).

A-kinase anchoring proteins (AKAPs) represent a family of adapter proteins that bind to the regulatory subunits of PKA and provide temporal-spatial control by localizing PKA in proximity to substrates and optimal pools of cAMP (Wong and Scott 2004). AKAP proteins show distinct tissue and subcellular distribution, such as the enrichment of AKAP79/150 in neuronal postsynaptic densities. In addition to binding to PKA, it also binds to PP2B and PKC (Dell'Acqua *et al.* 2002; Klauck *et al.* 1996), both of which regulate STEP (Snyder *et al.*, 2005 and unpublished data). Meanwhile, distinct combination of regulatory and catalytic subunits of PKA may also contribute to the region-specific regulation of STEP proteins (Gamm *et al.* 1996). It has been shown that different regulatory subunits of PKA display different sensitivity to cAMP levels. Moreover, RII β KO but not RI β KO mice show increased EtOH consumption (Thiele *et al.* 2000). Thus it would be important to determine whether AKAP79/150 provides a platform to facilitate the convergent regulation of STEP by these signaling pathways and distinct combination of PKA holoenzyme in a region or compartmental-specific manner.

The synergistic regulation of Fyn by STEP and PTP α is of interest. STEP dephosphorylates and inactivates Fyn directly (Nguyen *et al.* 2002) and we demonstrate a parallel pathway by which STEP dephosphorylates and suppresses PTP α function also leading to Fyn inactivation (Engen *et al.* 2008; Ingley 2008). On the other hand, Fyn may provide a positive feedback by phosphorylating PTP α at Y⁷⁸⁹ and enhancing its signaling, which is inhibited by STEP₆₁ at baseline and disinhibited upon ethanol exposure. Ethanol administration leads to activation of PKA (Ron and Messing 2013; Ortiz *et al.* 1995), and PKA phosphorylation of STEP isoforms results in the inability of STEP to interact with its substrates (Paul *et al.* 2000; Paul *et al.* 2003). At the same time, PKA phosphorylation of DARPP-32 results in inhibition of PP1, which is the phosphatase that dephosphorylates the PKA site in STEP isoforms (Paul *et al.* 2000). The inactivation of STEP₆₁ results in an increase in the Tyr phosphorylation of PTP α (Y⁷⁸⁹) and a decrease in the Tyr phosphorylation of Fyn at its inhibitory site (Y⁵³¹) by PTP α . In this example, the initial activation of PKA results in inactivation of STEP₆₁ and a subsequent translocation of PTP α to synaptic membranes and the full activation of Fyn.

In addition to ethanol-related disorders, the cross-talk between STEP and PTP α has been implicated in several neuropsychiatric disorders including schizophrenia (SZ). Previous findings indicate an elevation of STEP₆₁ level and activity in SZ postmortem brains and animal models of SZ (Carty *et al.* 2012). Interestingly, hypofunction of Fyn and PTP α are associated with neurobehavioral endophenotypes of SZ (Bjarnadottir *et al.* 2007; Takahashi *et al.* 2011), and the present results suggest a possible mechanism for these findings.

In summary, we show that PTP α is a novel substrate for STEP. The phosphorylation and inactivation of STEP₆₁ upon ethanol administration facilitates the translocation of PTP α to lipid rafts and subsequent activation of Fyn-NMDA receptor signaling (Fig. 7). Further studies are needed to investigate possible signaling pathways that underlie the specific phosphorylation and inactivation of STEP₆₁ in the DMS.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

This work was supported by NIH grants P50 AA012870, MH052711 and MH091037 (P.J.L). The authors thank Drs. Thomas Lanz and Thao Nguyen (Pfizer Research & Development, Cambridge, MA) for providing the lentiviral-STEP shRNA reagents.

Abbreviations

AAV1/2	adeno-associated virus of mixed serotype 1/2
AKAP	A-kinase anchoring protein
AMPA	α -amino-3-hydroxyl-5-methyl-4-isoxazole-propionate
CHL1	close homolog of L1
DIV	days in vitro
DLS	dorsolateral striatum
DMS	dorsomedial striatum
ERK	extracellular-signal regulated kinase
GST	glutathione S-transferase
IP	immunoprecipitation
KIM	kinase interacting motif
KO	knock out
MAPK	mitogen-activated protein kinase
NAc	nucleus accumbens
NCAM	neural cell adhesion molecule
NMDAR	N-methyl-D-aspartate receptor
PAGE	polyacrylamide electrophoresis
pNPP	<i>para</i> -nitrophenyl phosphate
PTPα	receptor-type Protein Tyrosine Phosphatase alpha
pyk2	proline-rich tyrosine kinase 2
SDS	sodium dodecyl sulfate
SH2 domain	Src homology 2 domain
shRNA	short hairpin RNA
STEP	STriatal-Enriched protein tyrosine Phosphatase
WT	wild type

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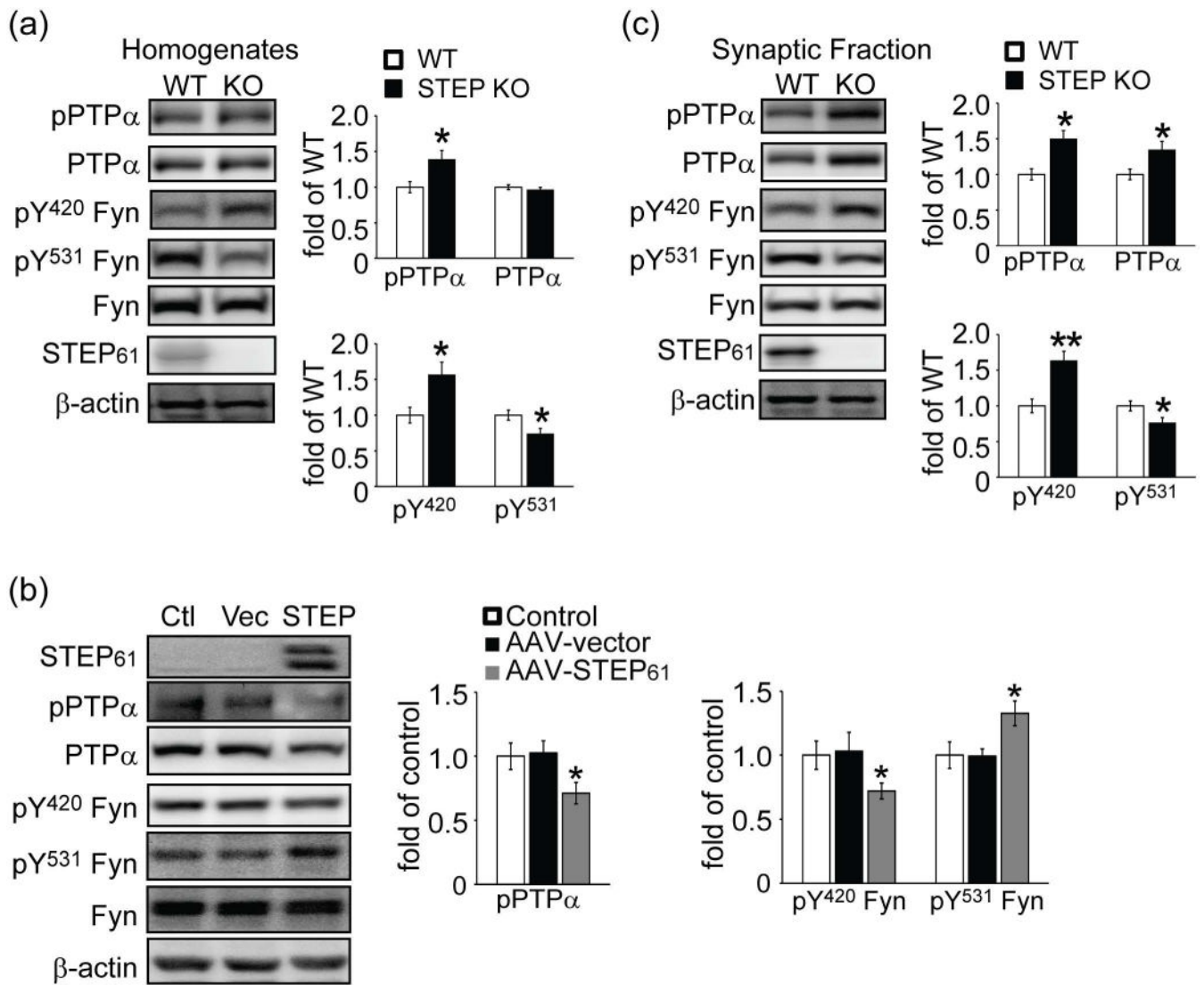


Figure 1. Phosphorylation level of PTPα at Tyr⁷⁸⁹ is elevated in STEP KO mouse striatum and decreased when STEP₆₁ is restored to STEP KO cultures. Tyrosine phosphorylation levels of PTPα (pY⁷⁸⁹), Fyn (pY⁴²⁰ and pY⁵³¹), and total protein levels were determined in total homogenates from wild-type (WT) and STEP KO (KO) mouse striatum (a), corticostriatal neurons from STEP KO mice with restoration of STEP₆₁ expression using AAV1/2-STEP₆₁ (b) or synaptic membrane fractions from wild-type (WT) and STEP KO (KO) mouse striatum (c) Quantification of phosphorylation levels were normalized to total protein levels and then to β-actin as a loading control. All data were expressed as mean ± SEM (**p* < 0.05, ***p* < 0.01, Student's *t*-test for (a) and (c), one-way ANOVA with Tukey's test for (b); *n* = 6).

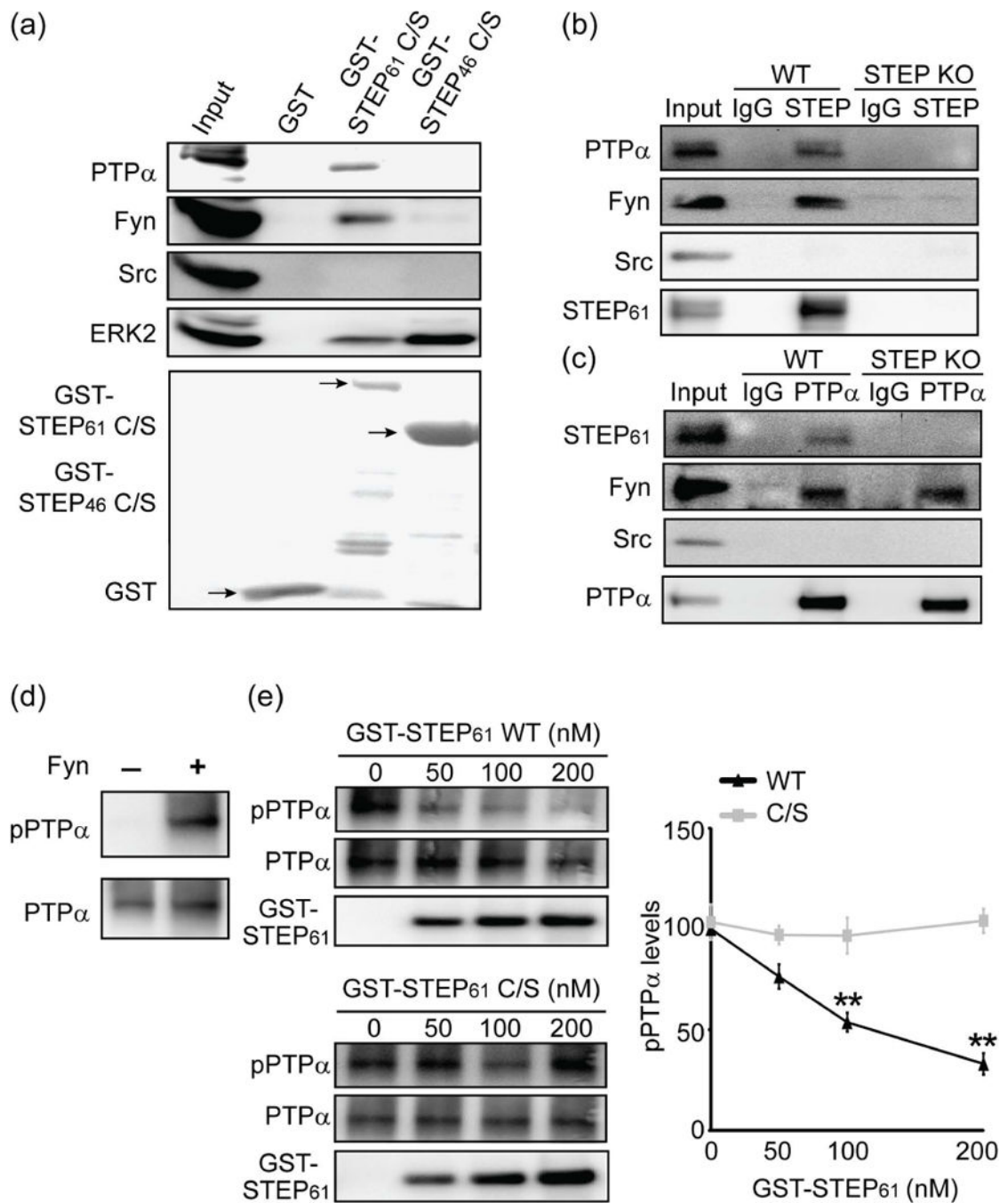


Figure 2. STEP₆₁ binds to and dephosphorylates PTP α at Tyr⁷⁸⁹. (a) The substrate-trapping (C472S) mutants STEP₆₁ C/S and STEP₄₆ C/S or GST tag alone were adsorbed to glutathione sepharose beads and incubated with mouse striatal homogenates. Bound proteins were visualized with specific antibodies as indicated in the figure. (b, c) STEP₆₁ is associated with PTP α in mouse striatum. WT or STEP KO mouse striatal lysates (300 μ g) were incubated with mouse IgG and anti-STEP (23E5) mouse monoclonal antibody (b) or goat IgG and anti-PTP α goat polyclonal antibody (c) overnight at 4 °C. Co-immunoprecipitation

of STEP interacting proteins (b) or PTP α interacting proteins (c) was probed with antibodies indicated in the figure. Thirty μ g of WT striatal lysates were used as input. Representative blots were shown from three independent experiments (n = 3). (d) Recombinant PTP α was phosphorylated by Fyn *in vitro*. (e) STEP₆₁ dephosphorylates PTP α at Tyr⁷⁸⁹. *In vitro* phosphorylated recombinant PTP α was incubated with active STEP₆₁ (WT) or inactive STEP₆₁ (C/S). The residual phosphorylation of PTP α at Y⁷⁸⁹ was assessed using a phospho-specific antibody. Data were expressed as mean \pm SEM (WT versus C/S at the same dose: ** $p < 0.01$, one-way ANOVA with *post hoc* Tukey's test; n = 4).

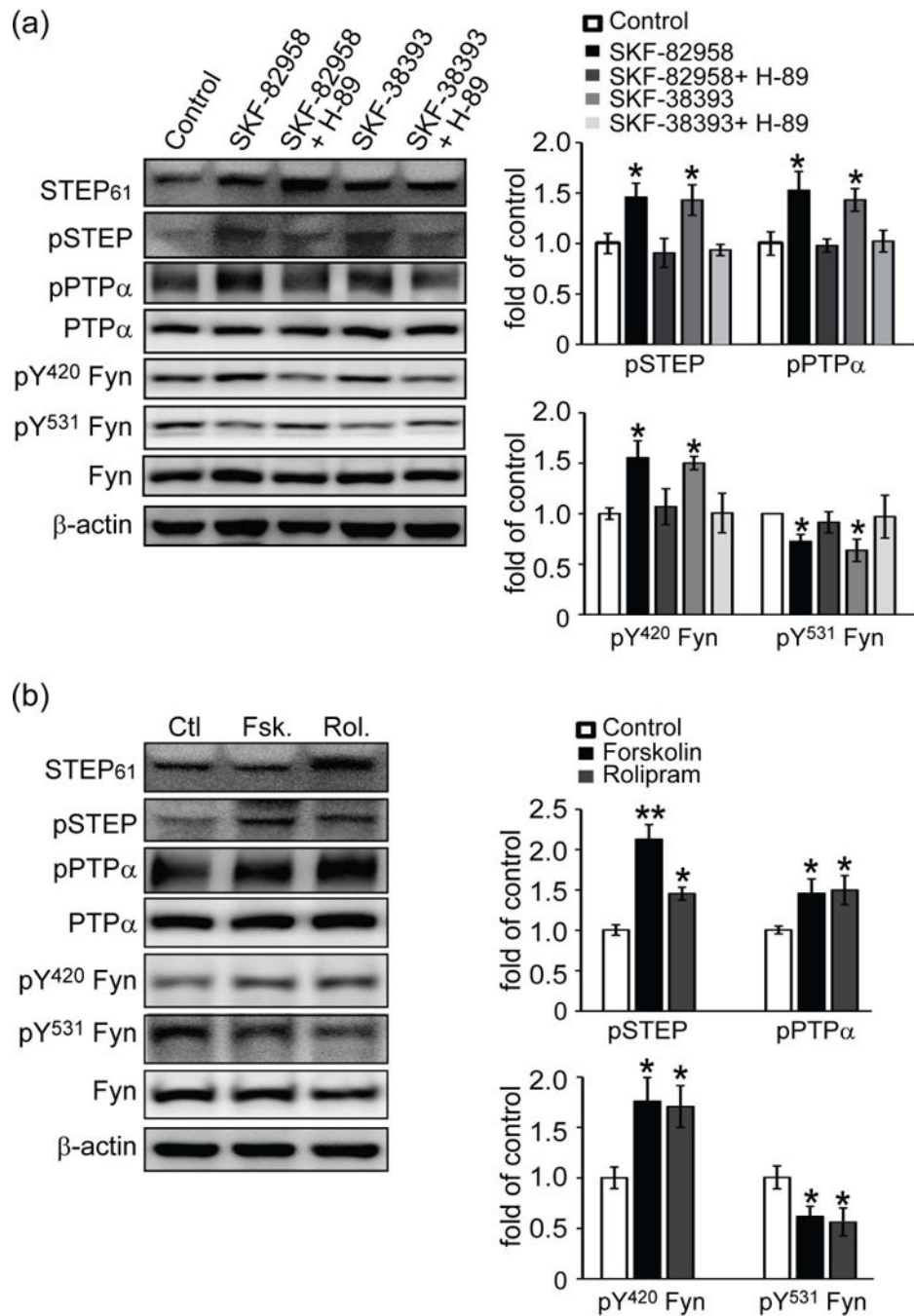


Figure 3. Inactivation of STEP₆₁ results in increased phosphorylation of PTPα. (a) D1 dopamine receptor activation leads to PKA-mediated phosphorylation and inactivation of STEP₆₁. Corticostriatal neurons were treated with SKF-82958 (10 μM) or SKF-38393 (10 μM) for 30 min. Some cultures were preincubated with H-89 (10 μM) for 30 min, followed by D1R agonists stimulations. (b) Inhibition of STEP₆₁ leads to increased phosphorylation of PTPα. Neurons were treated with forskolin (Fsk, 100 μM, 10 min) and rolipram (Rol, 1 μM, 30 min) prior to western blotting. Phospho-protein and total protein levels were assayed with

phospho-specific and pan-antibodies as indicated. Phospho-proteins were normalized to total protein levels and then to β -actin as a loading control. All data were compared to controls and expressed as mean \pm SEM and statistical significance was determined with one-way ANOVA with Tukey's test (* p < 0.05, ** p < 0.01; n = 4).

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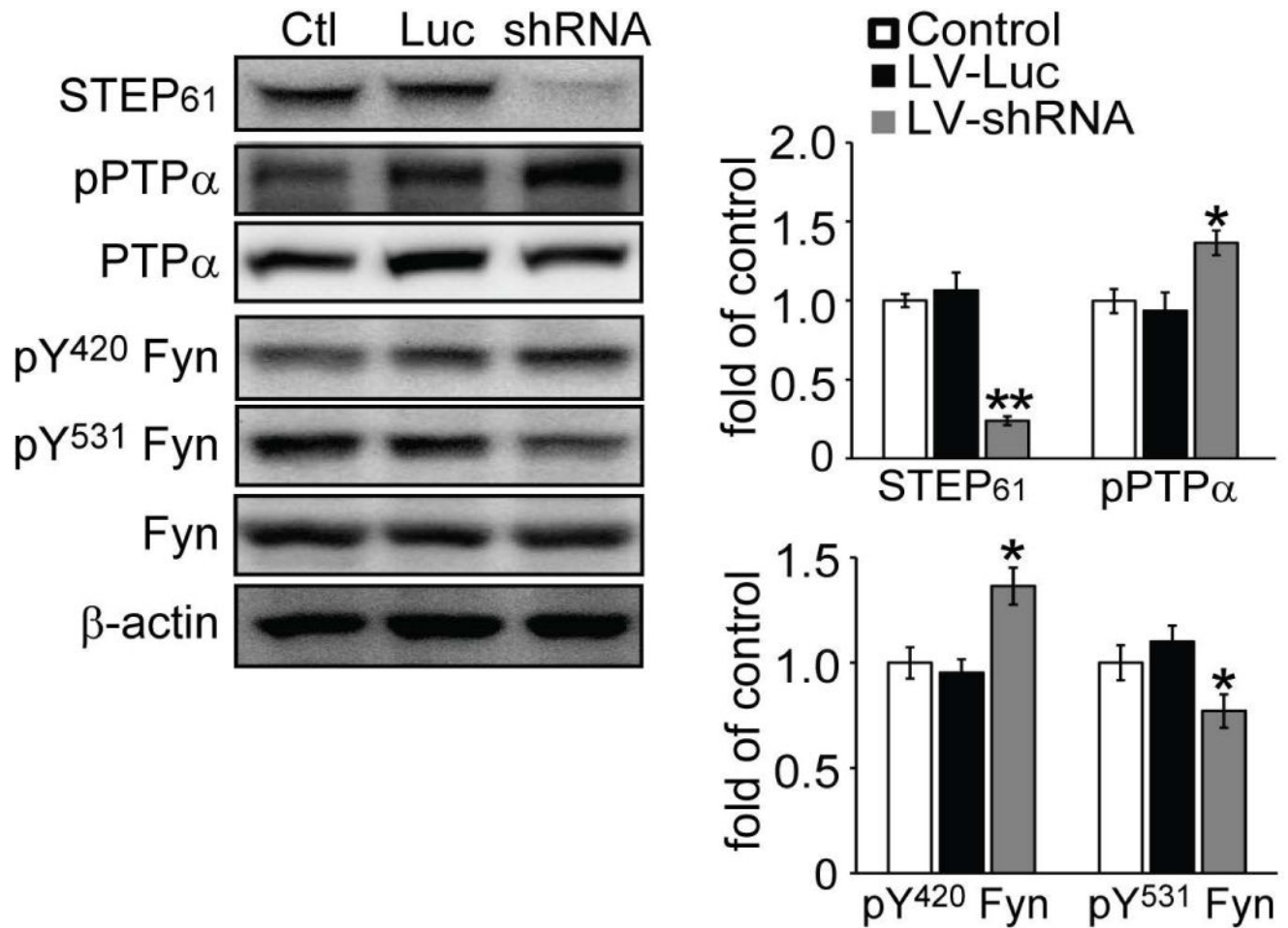


Figure 4.

STEP₆₁ knockdown results in increased PTP α phosphorylation at Tyr⁷⁸⁹ in corticostriatal cultures. Neuronal cultures were treated with lentivirus containing luciferase control (Luc) or STEP shRNA (shRNA) for 7 days. Neurons were lysed in RIPA buffer with protease inhibitors and phosphatase inhibitors and subjected to western blotting. STEP₆₁ and its substrates were probed with phospho-specific or pan-antibodies. Phospho-protein levels were normalized to total protein levels, and then to β -actin as a loading control. All data were compared to controls and expressed as mean \pm SEM and statistical significance was determined using one-way ANOVA with Tukey's test (* p < 0.05, ** p < 0.01; n = 6).

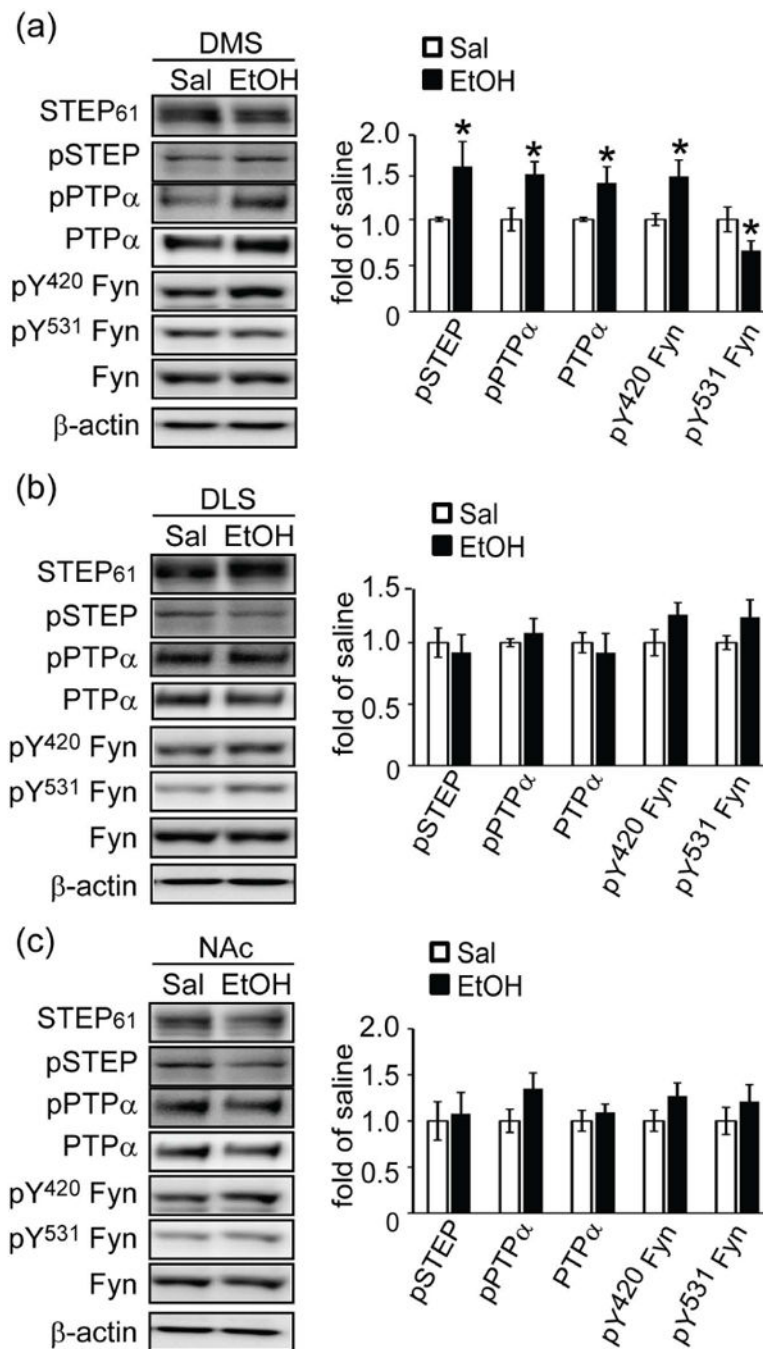


Figure 5. Acute ethanol administration results in phosphorylation and inactivation of STEP₆₁ and increased synaptic localization of PTP α in DMS. C57BL/6 mice (2–3 months) were injected with ethanol (EtOH) acutely (2 g/kg, i.p.) for 15 min. Mice brain regions DMS (a), DLS (b) and NAc (c) were dissected and crude synaptic membrane fractions were isolated and used for western blotting with phospho-specific and pan antibodies. Quantification of phosphorylation levels were normalized to total protein levels and then to β -actin as a loading control. All data were expressed as mean \pm SEM (* p < 0.05, Student's t -test; n = 5).

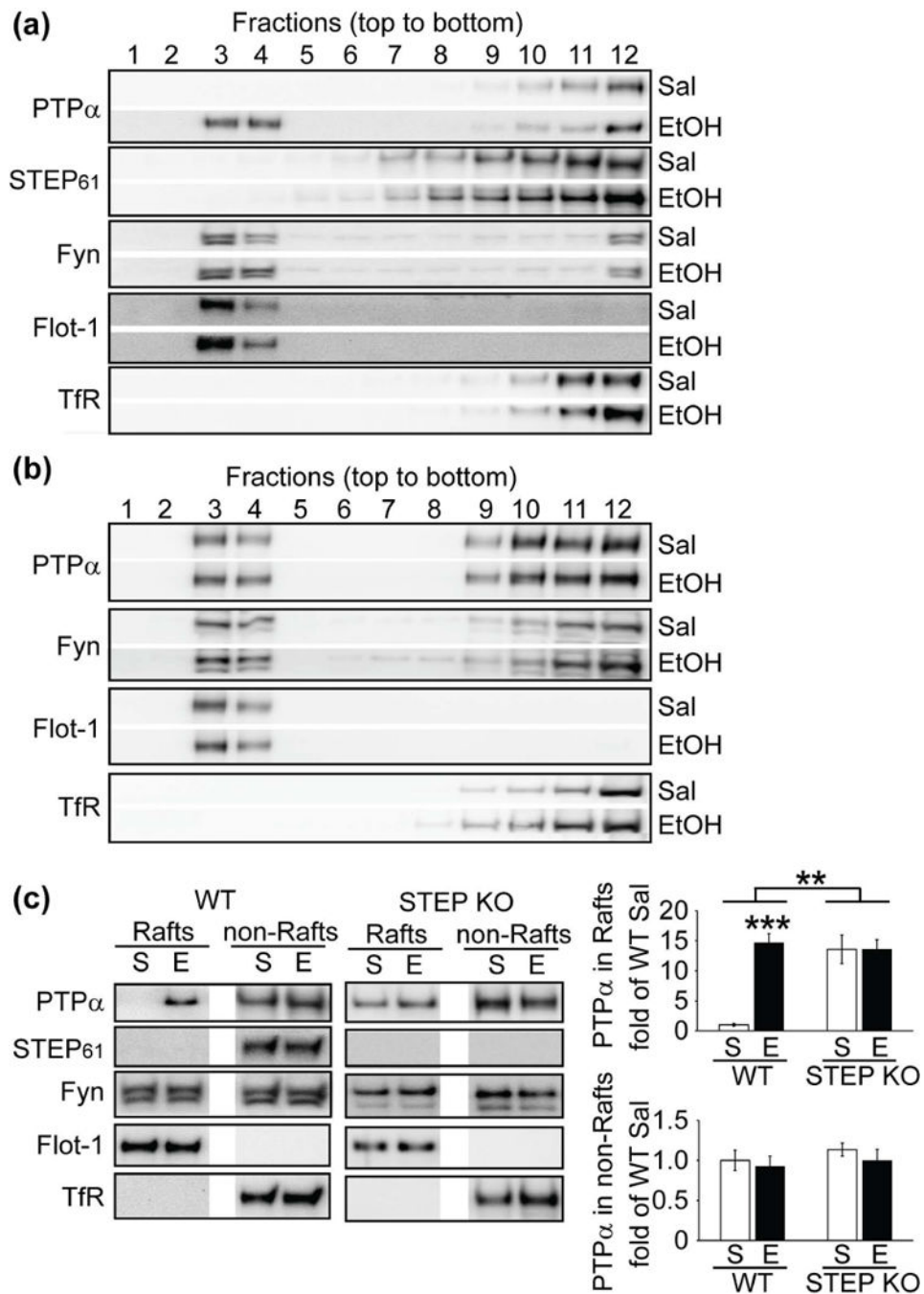


Figure 6. STEP₆₁ regulates translocation of PTP α into lipid rafts fraction in DMS upon acute ethanol administration. (a, b) WT (C57BL/6, 2–3 months) and STEP KO (C57BL/6 background) mice were injected with ethanol (EtOH) acutely (2 g/kg, i.p.) for 15 min. DMS was dissected out and subjected to sucrose gradient fractionation to obtain lipid rafts and non-rafts fraction. Distribution of PTP α , STEP₆₁ and Fyn in each fraction were probed with specific antibodies. Flotillin-1 (Flot-1) and transferrin receptor (TfR) were used as markers. (c) Distribution of PTP α , STEP₆₁ and Fyn in rafts fraction (fractions 3 and 4) and non-rafts

fraction (fractions 10–12) were probed with specific antibodies. Representative results were shown from 5 mice each group (n = 5). Data were expressed as mean \pm SEM (** $p < 0.01$, *** $p < 0.001$, two-way ANOVA with *post hoc* Tukey's test; n = 5).

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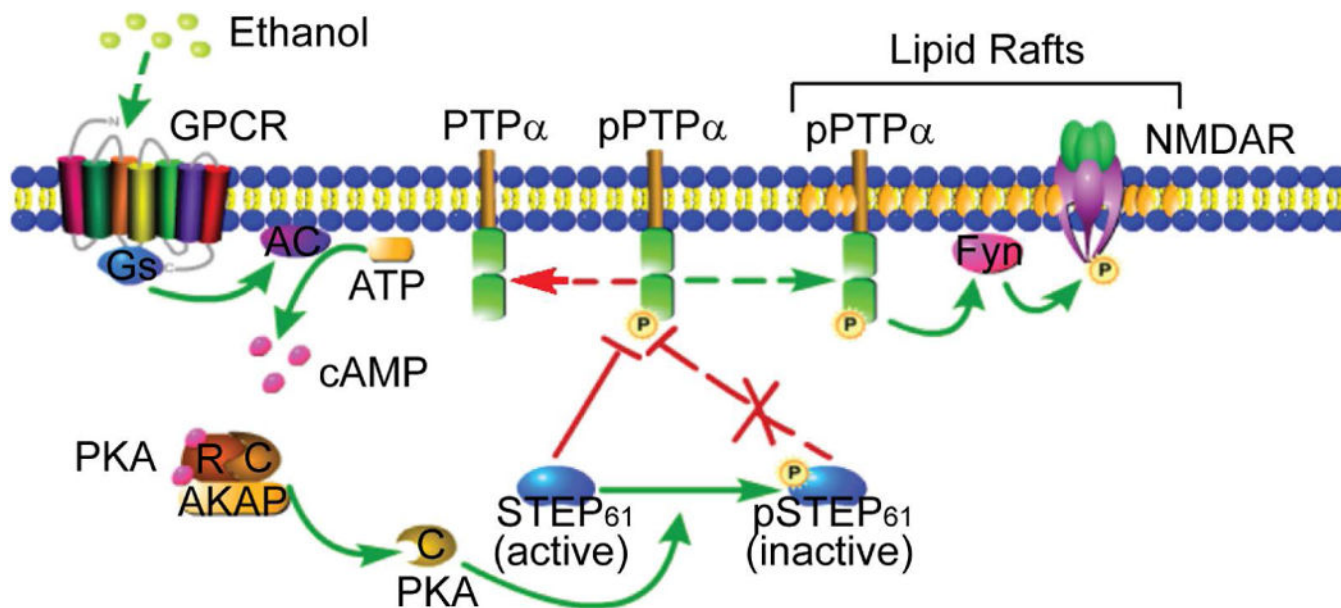


Figure 7. Schematic model of regulation of PTP α by STEP $_{61}$ during EtOH treatment in DMS. At basal conditions, active STEP $_{61}$ gates phosphorylation of PTP α and its translocation to the lipid rafts fractions where Fyn and NMDAR reside. Upon EtOH exposure, GPCR (such as D1R and A $_{2A}$ R) is activated, followed by activation of adenylate cyclase (AC) and production of cyclic AMP (cAMP). Binding of cAMP to the regulatory subunits (R) of PKA releases the active catalytic subunits (C) and subsequent phosphorylation of STEP $_{61}$ at a regulatory site (Ser 221), which is known to disrupt the interactions between STEP $_{61}$ and several of its substrates. Phosphorylation of STEP $_{61}$ (inactive) blocks its action on dephosphorylation of PTP α at Y 789 . Phosphorylated PTP α translocates to lipid rafts (maybe through binding to some adaptor proteins, with the mechanisms unclear), activates Fyn by dephosphorylating its inhibitory site (Y 531) and enhances NMDAR signaling, which is implicated in EtOH-related behaviors. The mechanisms underlying the region specificity (i.e. DMS versus DLS and NAc) remain unclear. We propose that distinct PKA regulatory and catalytic subunits and region-specific or compartment-specific distribution of AKAPs may be involved. GPCR, G-protein coupled receptor; D1R, dopamine D1 receptor; A $_{2A}$ R, adenosine A $_{2A}$ receptor; NMDAR, N-methyl-D-aspartate receptor; R, regulatory subunit; C, catalytic subunit; AKAP, A-kinase anchor protein; DMS, dorsomedial striatum; DLS, dorsolateral striatum; NAc, nucleus accumbens. This figure was created with the aid of the Pathway Builder Tool 2.0 (www.proteinlounge.com).